FIGURE 1A

```
  1 GAATTTGGGC CTCGAGGCCA AGAATGGGCG ACGAGGGCG GCGCCCAGCG CAGGCAGGAGC GCTGTCGCAT GGGGGCTCTCC
  1 CTTAAACCCG GAGCTCCGGT TCTTAACCGC TGCTCCCGCG CGGGGGTCGC GTCCGTCTCG CGACAGCGTA CCCCGAGAGG
  1                                                                      Me tGlyLeuSer

101 TGGAGCCCGC GACCTCCACT GCTGCTACTGG TGCTGTCGTT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACAGAG AACAGGTTTG
    ACCTCGGGCG CTGGAGGTGA CGACGATGACC ACGACAGCAA CACCGACGGT GAACCTCGTC CTTTGAGGGA ACGGTGTCTC TTGTCCAAAC
  5 TrpSerProA rgProProLe uLeuMetIle LeuLeuLeuV alLeuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal

201 TGAACAGCTG TACCCAGGCC AGAAAGAAAT GCGAGGCTAA TCCCGCTTGC AAGGCTGCCT ACCAGCACT GGGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
    ACTTGTCGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGGCGAACG TTCCGACGGA TGGTCGTGA CCCGGAGGACG TGGAGGTCAA ATTCGTCCGG
 39 AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro

301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
    CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT TTGTTGAGTC CTTGTCGAGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
 72 LeuProLeu GluGluSerA laMetSerAl aAspCysLeu AsnAsnSerS erLeuLeuAr gAsnSerSer LeuIleAspC ysArgCysHi sArgArgMet

401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCCG AAGCCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
    TTCGTGGTTC GATGGACAGA CCTGTAAATA ACCTGGCAAG TGGGACGGGC TTCGGAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTGTCACT
105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValSe rProTyrGlu AspThrValThr

501 CCAGCAAACC CTGGAAAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCAGACAA
    GGTCGTTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT AGACGGAGTT TAAACGATAC GACACATGAG AAGTCTGTT
139 SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuLy sPheAlaMet LeuCysThrL euHisAspLys

601 GTGGTGACCGC CTGGGCAAGG CCTACGGGGA GGGATCCGCT GCCAGGCGCA CCTCTGCCTA ATTTGCTATG CTTCAGGGCA
    CACACTGGCG GACCCGTTCC GGATGCCCCT CCCTAGGCGA CGGTCCGCGT GGAGACGGAT TAAACGATAC GAAGTCCCGT
172 CysAspAr gLeuArgLysA laTyrGlyGl uGlyIleArgC ysGlnArgHi sLeuCysLeu IleCysTyr LeuCysThrL euHisAspLys

701 GCAGAGTCCC ACGGTCAGGG TGTCCCTGTG CACCAGAGA TGCGGGCGGC GGCGGTAACAC CATCGCGCCC AGTTGCGCGG
    CGTCTCAGGG TGCCAGTCCC ACAGGGACAC GTGGTCTCT ACGCCCGCCG CCGCCATTGTG GTAGCGCGGG TCAACGCGCC
205 AlaGluSerH isAlaGlnGl yLeuLeuLeu CysProCysA laProGluAs pAlaGlyGlyC GlyGlyAsnTh rIleAlaPro SerCysAlaLeu

801 TGCCTTCTGT AACCCCCAAT TGCGGGAGCTT CTGCCGTGCG GACCCTTTGT GCAGATCACG CCTGATTGGG GCGGTAACAC ACTGTCATCC
    ACGGAAGACA TTGGGGGTTA ACGCCCTCGAA GACGGCACGC CTGGGAAACA CGTCTAGTGC GGACTAACCC CGCCATTGTG TGACAGTAGG
239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro

901 TATGGACATG ATACCTGTAG CTTGGGGACTT GTTGCAACTGA GCAGTTGCGCGG CATACCTGGG ACTGGATTGGG CCCCAAAACTT CATCAGCAAG
    ATACCTGTAC TATGGACATC GAACCCCTGAA CAACGTTGACT CGTCAGCGCC GTATGGACCC TGACCTAACC GGGGTTTTGAA GTAGTCGTTC
272 MetAspIle LeuGlyThrC ysAlaThrGl uGlnSerArg CysLeuArgA laTyrLeuGl yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys
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1001  GTCAACACTA CTGTTGCCTT AAGCTGCACC TGCCGGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGGAAAGGTC CTTCTCCCAG AACCCCTGCC
      CAGTTGTGAT GACAACGGAA TTCGACGTGG ACGGCCTCCGT CGCCGTTGGA TGTCCTGCTC ACACTTGTCG ACCTTTCCAG GAAGAGGGTC TTGGGGACGG
305   ValAsnThrT hrValAlaLe uSerCysThr CysArgArgG erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu

1101  TCGTGGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
      AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGTCTGT CGAGAAGAGG GTCCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCGTT
339   ValGluAl aIleAlaAla LysMetArgP heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG lnAsnSerAsn

1201  CCCTGCTCTG AGACTGCAGC CCAGGTACC CATTCTTTCT TTCCCTTGAT TCTGCTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
      GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGGGAACTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372   ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer PheSerIleL euProLeuIl eLeuLeuGln ThrLeuTrp

1301  CTTTGTCCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGGAGA GAACTCGCCA GCCTGGTGGAA GAAGAGGCAG CGTGCTACAC AGCAACCCGG
      GAAACAGGAG AGGTGGGTGTG GGTCTGACTA AACGTCGGAC ACCACCCTCT CTTGAGCGGT CGGACACCTT CTTCTCGCGTC GCACGATGTG TCGTTGGGCC

1401  AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGGCTAG TTTTCAAAAC
      TTGGTTGGTC CGTAAGGCGT CGTGTAGGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCCGATC AAAAGTTTGG

1501  TCCCTTGCCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTTGCCTTC TGTTCTGATG GTGATTAGCG GCTCACCTCC
      AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG CACTAATCGC CGAGTGGAGG

1601  AGCGGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTGACTG
      TCGCCGAAGAA GGACAAAGGG TCCTGGTGGG TCTCCGATTC CTTAGTCAGT AAGGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCACTGAC

1701  AGAAAAATGT TTCCTTTGTG TGGAAGGCTG GTGCGTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGGTG TCTTGACTGC TCTGCCAGGC
      TCTTTTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTCG GAGACTTACC TTCTATTTTT GGACGACCAC AGAACTGACG AGACGGTCCG

1801  AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGGG TCTCCTATTAC TGTCCCCAAA TTCCCCTAGT CCCTTGGGTC ATGATTAAAC
      TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT ACAGGGGTTT AAGGGGATCA GGGAACCCAG TACTAATTTG

1901  ATTTTGACTT AAAAAAAAAA AAAAAAAAAA AAAA
      TAAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTT
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FIGURE 1B

FIGURE 2

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rGFRa1    1  MFLATLYFALPLLDLLMSAEVSGG.........DRLDCVKASDQCLKEQSCSTKYRT
rGFRa2    1  MILANAFCLFFFLDETRSLASR..SSLQGSELHGWRPQVDCVRANELCAAESRYRT
mGFRa3    1  MGLWSPPPLLMICLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH

rGFRa1   49  RQCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCRCKRGMKKEKNCLRIYWSMYQ
rGFRa2   60  LRQCLAGRDRA....NTMLANKECQAALEVLQESPLYDCRCKRGMKKELQCLDIYWSIRL
mGFRa3   61  LGSCTSSLSRPLP-LEESAMSADCLEAAEQLRDCRCHRAMKHQATCLDIYWTVHP

rGFRa1  109  SEQ.GNDLEDSPYEPVNSRLSDIFRAVPFISDVFQQVEHISKGNNCLDAAKACNLDDTC
rGFRa2  115  GLTEGEEFYEASPYEPVTSRLSDIFRLASIFSGTGTDPAVSTKSNHCLDAAKACNLNDNC
mGFRa3  120  ARSLGDYEDVSPYEDTVTSKPWKMNSKLNMLK......PDSDLCKFAMLCTLHDKC

rGFRa1  168  KKYRSAYITPCTTSMSNEV-CNRKCHKALRQFFDKVPAKHSYGMLFCSC-..RDIACTER
rGFRa2  175  KKLRSSYISICNREISPTERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC-QDQACAER
mGFRa3  173  DRLRKAYGEACS....GIRCQRHLCLAQLRSFFEKAAESHAQGLLCPCAPEDAGGER

rGFRa1  225  RRQTIVPVCSYEERPNCLSQDSCKTNYICRSRLADFFTNCQPESRSVSNCLKENYAD
rGFRa2  233  RRQTILPSCSYEDKEKPNCLDLRSLCRTDHFHANCRASYRTITSCPADNYQA
mGFRa3  228  RRNTIAPSC-ALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHP-ATEQSR

rGFRa1  285  CLIAYSGLIGTIVMTPNYVVDS..SSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAT
rGFRa2  293  CLIGSYAGMIGFDMTPNYVDSNPTGIVSPWCNCRGSGNMEEECEKFLRDFTENPCLRNAI
mGFRa3  285  CLIRAYLGLIGTAMTPNFISK.-VNMIVALSCTCRGSGNLQDECEQLRSFSQNPCLVEAI

rGFRa1  343  QAFGNGSDVTMWQPAPPVQTTTTTAFRVKNKPFGPAGSENEIPTHVLPPCANLQAQK
rGFRa2  353  QAFGNGSDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDSTSLG--TSVITTCTSIQEQG
mGFRa3  343  AA.-......................

rGFRa1  403  EKSNMSGSTHLCLSDSDFGKDGLAGASSHITTKSMAAPPSICSSSPVCMLTALAACLSV
rGFRa2  410  LKANISKELSMCFTELTTNISPGSKKVIKLNSGISRARLSAALTALPLEMCTICAL----
mGFRa3  345  A.-.....KMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSICPLI

rGFRa1  463  SIAETS
mGFRa3  392  LLQTLW
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(handwritten) 464

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hGFRa3    1  M V R P L N P R P L P P V V L M L L L L L P P S P L P L A A G D P L P T E S R L M N S C L Q A R R K
mGFRa3    1  . . . M G L S W S P R P P L L M I L L L V L S L W . L P L G A G N S L A T E N R F V N S C T Q A R K K

hGFRa3   51  C Q A D P T C S A A Y H H L D S C T S S I S T P L P S E E P S V P A D C L E A A Q O L R N S S L I G
mGFRa3   48  C E A N P A C K A A Y Q H L G S C T S S L S R P L P L E E S A M S A D C L E A A E Q L R N S S L I O

hGFRa3  101  C M C H R R M K N Q V A C L D I Y W T V H R A R S L G N Y E L D V S P Y E D T V T S K P W K M N L S
mGFRa3   98  C R C H R R M K H Q A T C L D I Y W T V H P A R S L G D Y E L D V S P Y E D T V T S K P W K M N L S

hGFRa3  151  K L N M L K P D S D L C L K F A M L C T L N D K C D R L R K A Y G E A C S G P H C Q R H V C L R Q L
mGFRa3  148  K L N M L K P D S D L C L K F A M L C T L H D K C D R L R K A Y G E A C S G I R C Q R H L C L A Q L

hGFRa3  201  L T F F E K A A E P H A Q G L L L C P C A P N D R G C G E R R R N T I A P N C A L P P V A P N C L E
mGFRa3  198  R S F F E K A A E S H A Q G L L L C P C A P E D A G C G E R R R N T I A P S C A L P S V T P N C L O

hGFRa3  251  L R R L C F S D P L C R S R L V D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M
mGFRa3  248  L R S F C R A D P L C R S R L M D F Q T H C H P M D I L G T C A T E Q S R C L R A Y L G L I G T A M

hGFRa3  301  T P N F V S N V N T S V A L S C T C R G S G N L Q E E C E M L E G F F S H N P C L T E A I A A K M R
mGFRa3  298  T P N F I S K V N T T V A L S C T C R G S G N L Q D E C E Q L E R S F S Q N P C L V E A I A A K M R

hGFRa3  351  F H S Q L F S Q D W P H P T F A V M A H Q N E N P A V R P Q P W V P S L F S C T L P L I L L L S L W
mGFRa3  348  F H R Q L F S Q D W A D S T F S V V Q Q Q N S N P A L R L Q P R L P I L S F S I L P L I L L Q T L W
```

FIGURE 3

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48613    1  MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK
48614    1  MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK


48613   51  CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614   51  CQADPTCSAAYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG


48613  101  CMCHRRMKNQVACLDIYWTVHRARSL GNYELDVSPYEDTVTSKPWKMNLS
48614  101  CMCHRRMKNQVACLDIYWTVHRARSL . . . . . . . . . . . . . . . . . . . . . . . . .


48613  151  KLNMLKP DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614  127  . . . . . . . DSDLCLKFAMLCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL


48613  201  LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614  170  LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE


48613  251  LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614  220  LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM


48613  301  TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR
48614  270  TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMR


48613  351  FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
48614  320  FHSQLFSQDWPHPTFAVMAHQNENPAVRPQPWVPSLFSCTLPLILLLSLW
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FIGURE 4

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DNA48613.orf    1   ATGGTGCGCCCCCTGAACCGCGGACCGCTGCCGCCCGTAGTCCTGATGTT
GDNFRa1.orf     1   ................................................ATGTT
GDNFRa2.orf     1   ..........ATGATCTTGGCAAACGTCTTCTGCCTCTTCTTCTTTCT

DNA48613.orf   51   GCTGCTGCTGCTGCCGCCGTCGCCGCTGCCTCTCGCAGCCGGAGACCCCC
GDNFRa1.orf     6   CCTGGCGACCCTGTACTTCGCGCTGCCGGCTCTTGGACTTGCTCCTGTCGG
GDNFRa2.orf    39   AGACGAGACCCTCCGCTCTTTGGCCAGCCCTTCCTCCCTGCAGGGCCCCG

DNA48613.orf  101   TTCCCACAGAAAGCCGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAAG
GDNFRa1.orf    56   CCGAAGTGAGCGGCGGAGACCGCCTGGATTGCGTGAAAGCCAGTGATCAG
GDNFRa2.orf    89   AGCTCCACGGCTGGCGCCCCCCAGTGGACTGTGTCCGGGCCAATGAGCTG

DNA48613.orf  151   TGCCAGGCTGATCCCACCTGCAGTGCTGCCTACCACCACCTGGATTCCTG
GDNFRa1.orf   106   TGCCTGAAGGAGCAGAGCTGCAGCACCAAGTACCGCACGCTAAGGCAGTG
GDNFRa2.orf   139   TGTGCCGCCGAATCCAACTGCAGCTCTCGCTACCGCACTCTGCGGCAGTG

DNA48613.orf  201   CACCTCTAGCATAAGCACCCCACTGCCCT...CAGAGGAGCCTTCGGTCC
GDNFRa1.orf   156   CGTGGCGGGCAAGGAGACCAACTTCAGCCTGGCATCCGGCCTGGAGGCCA
GDNFRa2.orf   189   CCTGGCAGGCCGCGACCGCAACACCATGC..............TGGCCA

DNA48613.orf  248   CTGCTGACTGCCTGGAGGCAGCACAGCAACTCAGGAACAGCTCTTCTGATA
GDNFRa1.orf   206   AGGATGAGTGCCGCAGCGCCATGGAGGCCCTGAAGCAGAAGTCGCTCTAC
GDNFRa2.orf   224   ACAAGGAGTGCCAGGCGGCCTTGGAGGTCTTGCAGGAGAGCCCGCTGTAC

DNA48613.orf  298   GGCTGCATGTGCCACCGGCGCATGAAGAACCAGGTTGCCTGCTTGGACAT
GDNFRa1.orf   256   AACTGCCGCTGCAAGCGGGGTATGAAGAAGGAGAAGAACTGCCTGCGCAT
GDNFRa2.orf   274   GACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGCAGAT

DNA48613.orf  348   CTATTGGACCGTTCACCGTGCCCGCAGCCTTGGTAACTATGAGCTGGATG
GDNFRa1.orf   306   TTACTGGAGCATGTACCAGAGCCTGCAGGGAAATGATCTGCTGGAGGATT
GDNFRa2.orf   324   CTACTGGAGCATCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAG

DNA48613.orf  398   TCTCCCCCTATGAAG.....................ACACAGTGACCAGC
GDNFRa1.orf   356   CCCCATATGAACCAGTTA.................ACAGCAGATTGTCA
GDNFRa2.orf   374   CCTCCCCCTATGAGCCGGTGACCTCCCGCCTCTCGGACATCTTCAGGCTT

DNA48613.orf  427   AAACCCTGGAAAATGAATCTCAGCAAACTGAACATGCTCAAACCAGACTC
GDNFRa1.orf   388   GATATATTCCGGGTGGTCCCATTCATATCAGTGGAGCACATTCCCAAAGG
GDNFRa2.orf   424   GCTTCAATCTTCTCAGGGACAGGGGCAGACCCGGTGGTCAGCGCCAAGAG

DNA48613.orf  477   AGACCTCTGCCTCAAGTTTGCCATGCTGTGTACTCTCAATGACAAGTGTG
GDNFRa1.orf   438   GAACAACTGCCTGGATGCAAGCGAAGGCCTGCAACCTCGACGACATTTGCA
GDNFRa2.orf   474   CAACCATTGCCTGGATGCTGCCAAGGCCTGCAACCTGAATGACAACTGCA

DNA48613.orf  527   ACCGGCTGCGCAAGGCCTACGGGGAGGCGTGCTCCGGGCCCCACTG...C
GDNFRa1.orf   488   AGAAGTACAGGTCGGCGTACATCACCCCGTGCACCACCAGCGCGTGTC...C
GDNFRa2.orf   524   AGAAGCTGCGCTCCTCCTACATCTCCATCTGCAACCGCGAGATCTCGCCC

DNA48613.orf  574   CAGCGCCACCGTCTGCCTCAGGCAGCTGCTCACTTTCTTCGAGAAGGCCGC
GDNFRa1.orf   535   AATGATGTCTGCAACCGCCGCAAGTGCCACAAGGCCCTCCGGCAGTTCTT
GDNFRa2.orf   574   ACCGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGCGCCAGTTCTT

DNA48613.orf  624   CGAG......CCCCACGCGCAGGGCCTGCTACTGTGCCATGTGCCCCCA
GDNFRa1.orf   585   TGACAAGGTCCCCGGCCAAGCACAGCTACGGAATGCTCTTCTGCTCCTGCC
GDNFRa2.orf   624   CGACCGGGTGCCCAGCGAGTACACCTACCGCATGCTCTTCTGCTCCTGCC

DNA48613.orf  668   ACGACCGGGGCTGCGGGGAGCGCCGGCGCAACACCATCGCCCCCAACTGC
GDNFRa1.orf   635   GGGACATCGCCTGCACAGAGCGAGGCGGACAGACCATCGTGCCTGTGTGC
GDNFRa2.orf   674   AAGACCAGGCGGTGCGCTGAGCGCCGCCGCGGCAAACCATCCTGCCCAGCTGC
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FIGURE 5A

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DNA48613.orf   718  G C G C T G C C · · · G C C T G T G G C C C C C A A C T G C C T G G A G C T G C G G C G C C T C T G
GDNFRa1.orf    685  T C C T A T G A A G A G A G G G A G A A G C C C A A C T G T T T G A A T T T G C A G G A C T C C T G
GDNFRa2.orf    724  T C C T A T G A G G A C A A G G A G A A G C C C A A C T G C C T G G A C C T G C G T G G C G T G T G

DNA48613.orf   765  C T T C T C C G A C C C G C T T T G C A G A T C A C G C C T G G T G G A T T T C C A G A C C C A C T
GDNFRa1.orf    735  C A A G A C G A A T T A C A T C T G C A G A T C T T C G C C T T G C G G A T T T T T T T A C C A A C T
GDNFRa2.orf    774  C C G G A C T G A C C A C C T G T G T C G G T C C C G G C T G G C C G A C T T C C A T G C C A A T T

DNA48613.orf   815  G C C A T C C C A T G G A C A T C C T A G G A A C T T G T G C A A C A G A G C A G T C C A G A · · ·
GDNFRa1.orf    785  G C C A G C C A G A G T C A A G G T C T G T C A G C A G C T G T C T A A A G G A A A A C T A C G C T
GDNFRa2.orf    824  G T C G A G C C T C C T A C C A G A C G G T C A C C A G C T G C C C T G C G G A C A A T T A C C A G

DNA48613.orf   862  · · · T G T C T A C G A G C A T A C C T G G G G C T G A T T G G G A C T G C C A T G A C C C C C A A
GDNFRa1.orf    835  G A C T G C C T C C T C G C C T A C T C G G G G C T T A T T G G C A C A G T C A T G A C C C C C A A
GDNFRa2.orf    874  G C G T G T C T G G G C T C T T A T G C T G G C A T G A T T G G G T T T G A C A T G A C A C C T A A

DNA48613.orf   909  C T T T G T C A G C A A T G T C A · · · · · · A C A C C A G T G T T G C C T T A A G C T G C A C C T
GDNFRa1.orf    885  C T A C A T A G A C T C C A G T A · · · · · · G C C T C A G T G T G G C C C C A T G G T G T G A C T
GDNFRa2.orf    924  C T A T G T G G A C T C C A G C C C C A C T G G C A T C G T G G T G T C C C C C T G G T G C A G C T

DNA48613.orf   953  G C C G A G G C A G T G G C A A C C T G C A G G A G G A G T G T G A A A A T G C T G G A A G G G T T C
GDNFRa1.orf    929  G C A G C A A C A G T G G G A A C G A C C T A G A A G A G T G C T T G A A A T T C T T G A A T T T C
GDNFRa2.orf    974  G T C G T G G C A G C G G G A A C A T G G A G G A G G A G T G T G A G A A G T T C C T C A G G G A C

DNA48613.orf  1003  T T C T C C C A C A A C C C C T G C C T C A C G G A G G C C A T T G C A G C T A A G A T G C G T T T
GDNFRa1.orf    979  T T C A A G G A C A A T A C A T G T C T T A A A A T G C A A T T C A A G C C T T T G G C A A T G G
GDNFRa2.orf   1024  T T C A C C G A G A A C C C A T G C C T C G G A A C G C C A T C C A G G C C T T T G G C A A C G G

DNA48613.orf  1053  T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
GDNFRa1.orf   1029  C T C C G A T G T G A C C G T G T G G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
GDNFRa2.orf   1074  C A C G G A C G T G A A C G T G T C C C C A A A A G G C C C C T C G T T C C A G G C C A C C A C A G G

DNA48613.orf  1103  T G G C A C A C C A G A A T G A A A A C C C T G C T G T G A G G C C A C A G C C C T G G G T G C C C
GDNFRa1.orf   1079  C C A C T A C C A C C A C T G C C C T C C G G G T T A A G A A C A A A C C C C T G G G G C C A G C A
GDNFRa2.orf   1124  C C C C T C G G G T G G G A G A A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

DNA48613.orf  1153  T C T C T T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
GDNFRa1.orf   1129  G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T T G C C A C C G T G T G C A A A T T T
GDNFRa2.orf   1174  A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

DNA48613.orf  1203  G · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · · ·
GDNFRa1.orf   1179  A C A G G C A C A G A A G C T G A A A T C C A A T G T G T C G G G C A A T A C A C A C C T C T G T A
GDNFRa2.orf   1224  G G G G C T G A A G G C C A A C A A C T C C A A A G A G T T A A G C A T G T G C T T C A C A G A G C

GDNFRa1.orf   1229  T T T C C A A T G G T A A T T A T G A A A A A G A A G G T C T C G G T G C T T C C A G C C A C A T A
GDNFRa2.orf   1274  T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

GDNFRa1.orf   1279  A C C A C A A A A T C A A T G G C T G C T C C T C C A A G C T G T G G T C T G A G C C C A C T G C T
GDNFRa2.orf   1324  G G C C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T G T C C T

GDNFRa1.orf   1329  G G T C C T G G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A A C A G A A A C A T
GDNFRa2.orf   1374  G A T G C T G A A A C A G G C C T T G T A G · · · · · · · · · · · · · · · · · · · · · · · · · · ·

GDNFRa1.orf   1379  C A T A G
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FIGURE 5B

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DNA48613   1   MVRPLNPRPLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRK
GDNFRa1    1   MFLAT...LYFAL..PLLDLLLSA-.EVSGGD.....RL..DCVKASDQ
GDNFRa2    1   MILANVFCLFFFLDETLRSLASPS..SLQGPELHGWRPPV..DCVRANEL

DNA48613   51  CQADPTCSAAYHHLDSCTSSISTPLP.SEEPSVPADCLEAAQQLRNSSLI
GDNFRa1    36  CLKEQSCSTKYRTLRQCVAGKETNFSLASGLEAKDECRSAMEALKQKSLY
GDNFRa2    47  CAAESNCSSRYRTLRQCLAGRDRN.....TMLANKECQAALEVLQESPLY

DNA48613   100 GCMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTVTSKPWKMNL
GDNFRa1    86  NCRCKRAGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRV
GDNFRa2    92  DCRCKRAGMKKELQCLQIYWSIHLGLTEGEEFYEASPYEPVTSRLSDIFRL

DNA48613   150 SKL........NMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACS.....
GDNFRa1    135 VPFIS...VEHI..PKGNNCLDAAKACNLDDICKKYRSAYITPCTTSVS.
GDNFRa2    142 ASIFSGTGADPVVSAKSNHCLDAAKACNLNDNCKKLRSSYISICNREISP

DNA48613   188 GPHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAP
GDNFRa1    179 NDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC..RDIACTERRRQTIVP
GDNFRa2    192 TERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC..QDQACAERRRQTILP

DNA48613   238 NCALPPVA.PNCLELRRLCFSDPLCRSRLVDFQTHCHP.MDILGTCATEQ
GDNFRa1    227 VCSYEEREKPNCLNLQDSCKTNYICRSRLADFFTNCQPESRSVSSCLKEN
GDNFRa2    240 SCSYEDKEKPNCLDLRGVCRTDHLCRSRLADFHANCRASYQTVTSCPADN

DNA48613   286 .SRCLRAYLGLIGTAMTPNFVSNV..NTSVALSCTCRGSGNLQEECEMLE
GDNFRa1    277 YADCLLAYSGLIGTVMTPNYIDSS..SLSVAPWCDCSNSGNDLEECLKFL
GDNFRa2    290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCSCRGSGNMEEECEKFL

DNA48613   333 GFFSHNPCLTEAIAA.................KMRFHSQLFS
GDNFRa1    325 NFFKDNTCLKNAIQAFGNGSDVTVWQPAFPVQTTTATTTTALRVKNKPLG
GDNFRa2    340 RDFTENPCLRNAIQAFGNGTDVNVSPKGPSFQATQAPRVEKTPSLPDDLS

DNA48613   358 Q.........DWPHPTFAVMAHQNENPAVRPQ.................
GDNFRa1    375 PAGSENEIPTHVLPPCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASS
GDNFRa2    390 DSTS...LGTSVITTCTSVQEQGLKANNSKELSMCFT..ELTTNIIPGSN

DNA49613   381 ....PWVPSLFSCTLPLILLLSLW...........
GDNFRa1    425 HITTKSMAAPPSCGLSPLLVLVVTALSTLLSLTETS
GDNFRa2    435 KVIKPNSGPSRARPSAALTVLSVLMLKQAL......
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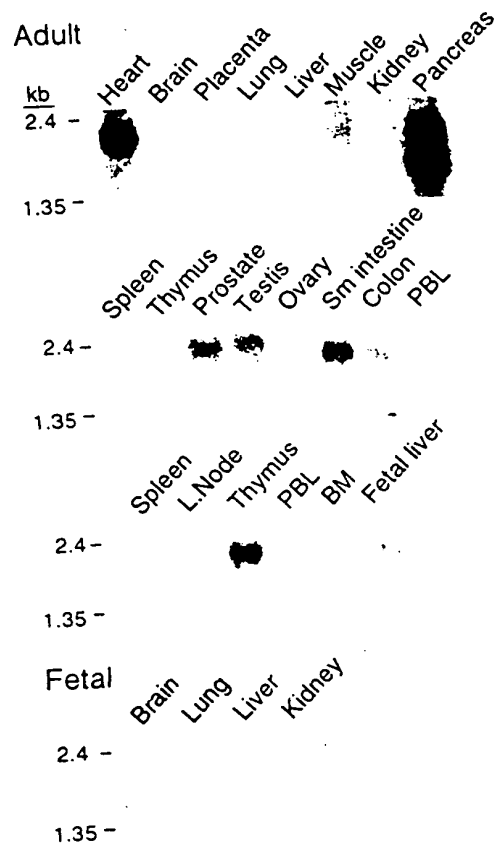
FIGURE 6

protein alignment

Adult

kb
2.4 –
1.35 –

Heart Brain Placenta Lung Liver Muscle Kidney Pancreas

Spleen Thymus Prostate Testis Ovary Sm intestine Colon PBL

2.4 –
1.35 –

Spleen L.Node Thymus PBL BM Fetal liver

2.4 –
1.35 –

Fetal

Brain Lung Liver Kidney

2.4 –
1.35 –

NORTHERN BLOTS
FIGURE 7

GFRα1   GFRα2   GFRα3

FIGURE 8

Binding to Rat GFRa1-IgG

FIG. 9A

absorbance 490 nm

rat GDNF	
huNTN	
huPSP	

receptor conc. ng/ml

Binding to Human GFRa2-IgG

FIG. 9B

absorbance 490 nm

receptor conc. ng/ml

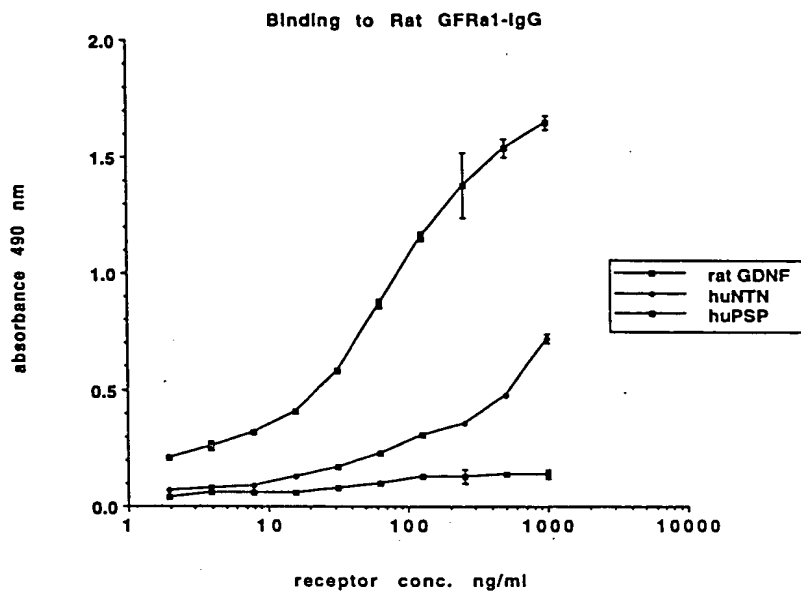**Binding to Human GFRa3-IgG**
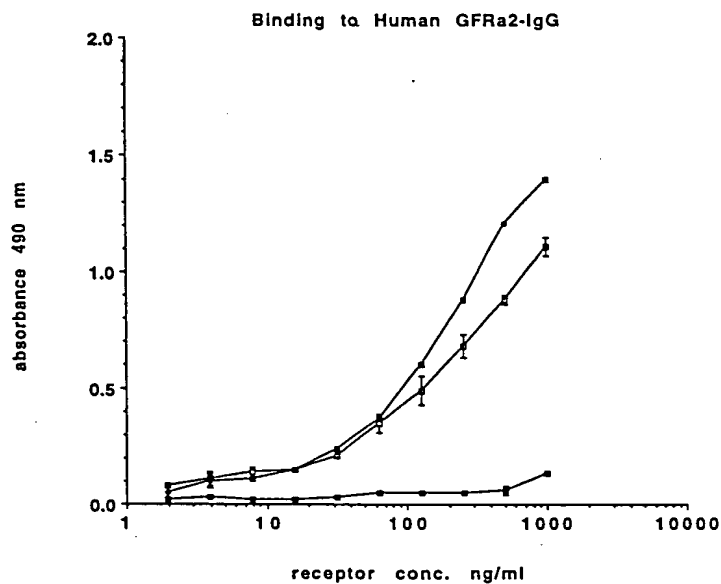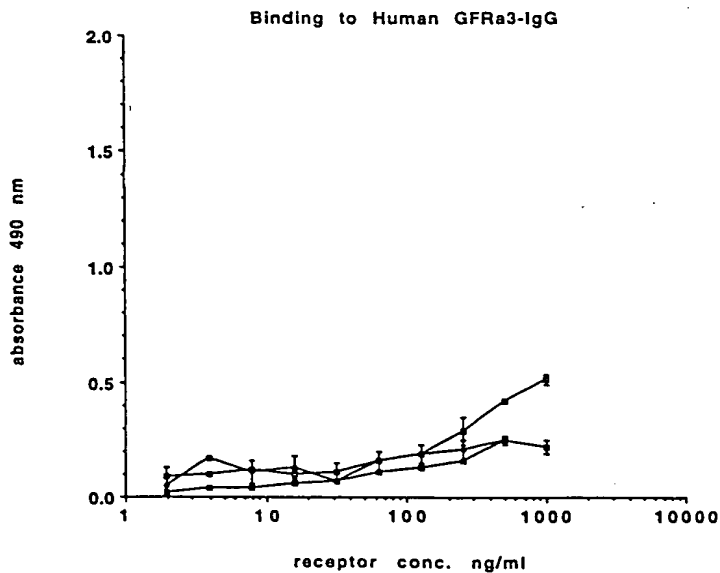
FIG. 9C

absorbance 490 nm

receptor conc. ng/ml

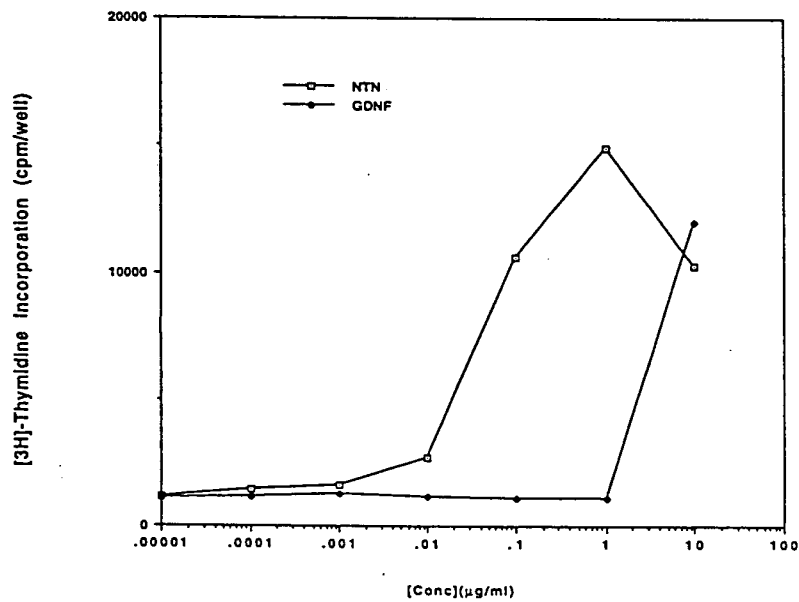Proliferation of Ba/F3-GFRaβ-mpl cells in response to NTN and GDNF

FIGURE 10

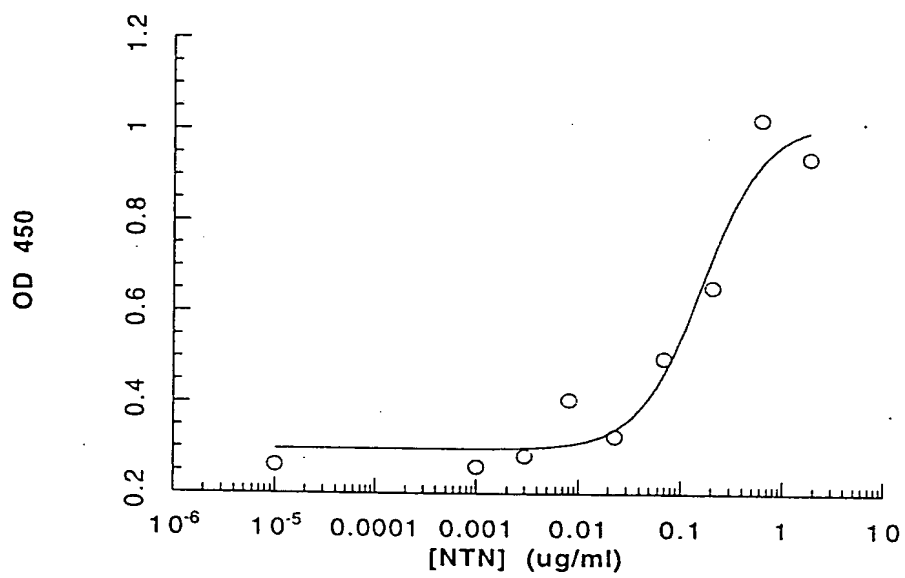Phosphorylation of GFRa2-Rse in response to NTN

FIGURE 11

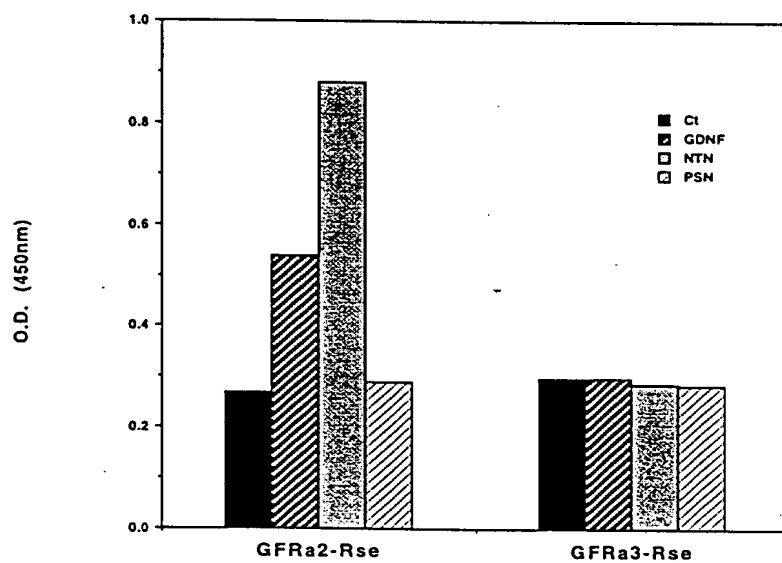**Stimulation of GFRa2 and GFRa3 by GDNF, NTN and PSN**

FIGURE 12

FIGURE 13

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

ug/ml	3C8	5B6	2272
1	1.409	1.211	1.463
0.4	1.791	1.600	1.511
0.16	1.684	1.267	0.915
0.064	1.017	0.749	0.562
0.0256	0.589	0.490	0.439
0.01024	0.427	0.406	0.371
0.004096	0.370	0.392	0.363
0	0.357	0.369	0.372

2, 1.8, 1.6, 1.4, 1.2, 1, 0.8, 0.6, 0.4, 0.2, 0